Abstract

The present invention is directed to a method for detecting a target nucleic acid sequence. The method may employ both an amplification procedure and a detection procedure. Amplification is accomplished through the use of a plurality of pairs of nucleic acid amplification probes, wherein the member probes of each pair of amplification probes are complementary to each other with at least one same hybridizing member of each pair of amplification probes also being complementary to a given portion of the target nucleic acid sequence, which acts as a template. The hybridizing members of each pair of amplification probes hybridize to the target sequence in a contiguous manner, sufficiently adjacent to each other to enable the probes to be joined together to form an amplification product. Once the hybridizing amplification probes are joined, the completed amplification product can be separated by denaturation, and the process repeated, until a sufficient quantity of the target nucleic acid sequence is produced to result in measurable signal in the selected assay. Where three or more pairs of amplification probes are employed, the amplification product may be specifically detected using two or more detection probes, wherein each detection probe is complementary to a portion of each of two adjacently situated amplification probe segments of the amplification product. The correctly assembled amplification product serves as a template in a manner similar to that served by the target nucleic acid sequence in the amplification procedure. The detection probes hybridize to the amplification product sufficiently adjacent to each other to enable the hybridized detection probes to interact with each other to ultimately produce a detectable signal.